

## SEQUENCE LISTING

<110> SAKI, Mayumi

NONAKA, Hiromi

MIYAJI, Hiromasa

HIURA, Naoko

MANABE, Haruhiko

MATSUMURA, Tsutsomu

ARAI, Hitoshi

SASAKI, Katsutoshi

KOBATAKE, Choei

IIDA, Kyoichiro

KUBOYAMA, Takeshi

<120> AGENT FOR PREVENTION AND/OR TREATMENT OF ASTHMA

<130> 506.44792X00

<140> 10/525,326

<141> 2005-02-22

<150> JP 2002/241523

<151> 2002-08-22

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 1

tcgacaaata aagcaatagc atcacaaatt tcacaaataa agcatttttt tcaa 54

<210> 2

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 2

tgcattgaaa aaaatgcttt atttgtgaaa tttgtgatgc tattgcttta ttg 54

<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 3

tgcattctag ttgtggtttg tccaaactcg agcccgggg 39

<210> 4

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 4

gtacccccgg gctcgagttt ggacaaacca caactagaa

39

<210> 5

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 5

tcgacggtat cgattcgact gacgtcatatc ttgacgtcac

40

<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 6

tcgagtgacg tcaagtatga cgtcagtcga atcgataccg

40

<210> 7

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 7

gccccagaag ctttaagtgcc caccatggg

29

<210> 8

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 8

gttcattgtg gcggccgcag catcttcagc tgc

33

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 9

cggagactct agagggtata taatg

25

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 10

ctaatacgac tcactatagg g

21

<210> 11

<211> 362

<212> PRT

<213> Homo sapiens

<400> 11

Met Gly Asn His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp  
1 5 10 15

His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu  
20 25 30

Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln  
35 40 45

Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu  
50 55 60

Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His  
65 70 75 80

Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile  
85 90 95

Phe Tyr Thr Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser  
100 105 110

Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu  
115 120 125

Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr  
130 135 140

Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg  
145 150 155 160

Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly  
165 170 175

Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe  
180 185 190

Pro Trp Ala Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val  
195 200 205

Arg Gly Ser Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg  
210 215 220

Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr  
225 230 235 240

His Val Leu Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp  
245 250 255

Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu  
260 265 270

Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu  
275 280 285

Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu  
290 295 300

Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser  
305 310 315 320

Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys  
325 330 335

Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln  
340 345 350

Val Gln Leu Lys Met Leu Pro Pro Ala Gln  
355 360

<210> 12

<211> 2932

<212> DNA

<213> Homo sapiens

<400> 12

```
ctgcagtcag gcggtgaact gacttcatcc caatccctca gccccacca ggaccagtct 60
ggagtccctc cctgcccccc attgaaatTT ccttccgTc cccaaactta cctctgatct 120
agaccttact cacctccttc ctgtttccta agactccttc ctgccgtcca cagaccgagc 180
cttttatctt tgtccaccct gtgccagaca cctccttttc cagaaccttc tccttactgg 240
tgaccttact tatctctgtt gctttctggg gtcctaggaa atgccagcac tcccaccac 300
attgcctgaa ctttccaaca ctccctagct gcgctgtgtc ctatctcaac acttcctcat 360
gtatttcttg tgtcttctag aacattcccc cgccattatt acttcaatat ggctacacat 420
acttcctaatt tgccctgcaa accatctcct tctcaccatt gccagcgat gctttcgtct 480
cctccataaa cactcccgga gaccaatTTT tgtgtcacc ccatactccc tcgttgacac 540
actgactcca tacataacct ccttgaaaaa cctctttatt aatctacca tcctccagac 600
ttccctcctg tcataattcc atccctcctc caacttttcc ctctcaagct ctgcccttcc 660
cagcccagcc cagcctaccc aacctcatct cttccctgta gaccacatcc caccatgttc 720
ccctgagcct ccaaggaagg ggctcagggg gccccatggc ctcccgtccc ctgtggcccc 780
acagcccccg tgggccaggg gaagcgcccc agaagccgaa gtgcccacc atg ggc aac 838
```

Met Gly Asn

1

```
cac acg tgg gag ggc tgc cac gtg gac tcg cgc gtg gac cac ctc ttt 886
His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp His Leu Phe
```

5

10

15

```
ccg cca tcc ctc tac atc ttt gtc atc ggc gtg ggg ctg ccc acc aac 934
Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu Pro Thr Asn
```

20

25

30

35

```
tgc ctg gct ctg tgg gcg gcc tac cgc cag gtg caa cag cgc aac gag 982
Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln Arg Asn Glu
```

40

45

50

```
ctg ggc gtc tac ctg atg aac ctc agc atc gcc gac ctg ctg tac atc 1030
```

Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu Leu Tyr Ile	
55 60 65	
tgc acg ctg ccg ctg tgg gtg gac tac ttc ctg cac cac gac aac tgg	1078
Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His Asp Asn Trp	
70 75 80	
atc cac ggc ccc ggg tcc tgc aag ctc ttt ggg ttc atc ttc tac acc	1126
Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile Phe Tyr Thr	
85 90 95	
aat atc tac atc agc atc gcc ttc ctg tgc tgc atc tcg gtg gac cgc	1174
Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser Val Asp Arg	
100 105 110 115	
tac ctg gct gtg gcc cac cca ctc cgc ttc gcc cgc ctg cgc cgc gtc	1222
Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu Arg Arg Val	
120 125 130	
aag acc gcc gtg gcc gtg agc tcc gtg gtc tgg gcc acg gag ctg ggc	1270
Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr Glu Leu Gly	
135 140 145	
gcc aac tcg gcg ccc ctg ttc cat gac gag ctc ttc cga gac cgc tac	1318
Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg Asp Arg Tyr	
150 155 160	
aac cac acc ttc tgc ttt gag aag ttc ccc atg gaa ggc tgg gtg gcc	1366
Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly Trp Val Ala	
165 170 175	
tgg atg aac ctc tat cgg gtg ttc gtg ggc ttc ctc ttc ccg tgg gcg	1414
Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe Pro Trp Ala	
180 185 190 195	
ctc atg ctg ctg tcg tac cgg ggc atc ctg cgg gcc gtg cgg ggc agc	1462
Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val Arg Gly Ser	
200 205 210	



gtg tcc acc gag cgc cag gag aag gcc aag atc aag cgg ctg gcc ctc	1510
Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg Leu Ala Leu	
215 220 225	
agc ctc atc gcc atc gtg ctg gtc tgc ttt gcg ccc tat cac gtg ctc	1558
Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr His Val Leu	
230 235 240	
ttg ctg tcc cgc agc gcc atc tac ctg ggc cgc ccc tgg gac tgc ggc	1606
Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp Asp Cys Gly	
245 250 255	
ttc gag gag cgc gtc ttt tct gca tac cac agc tca ctg gct ttc acc	1654
Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu Ala Phe Thr	
260 265 270 275	
agc ctc aac tgt gtg gcg gac ccc atc ctc tac tgc ctg gtc aac gag	1702
Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu Val Asn Glu	
280 285 290	
ggc gcc cgc agc gat gtg gcc aag gcc ctg cac aac ctg ctc cgc ttt	1750
Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu Leu Arg Phe	
295 300 305	
ctg gcc agc gac aag ccc cag gag atg gcc aat gcc tcg ctc acc ctg	1798
Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser Leu Thr Leu	
310 315 320	
gag acc cca ctc acc tcc aag agg aac agc aca gcc aaa gcc atg act	1846
Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys Ala Met Thr	
325 330 335	
ggc agc tgg gcg gcc act ccg ccc tcc cag ggg gac cag gtg cag ctg	1894
Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln Val Gln Leu	
340 345 350 355	
aag atg ctg ccg cca gca caa tga accccgagtg gcacagaatc cccagttttc	1948

Lys Met Leu Pro Pro Ala Gln

360

```
ccctctcatc ccacagtecc ttctctcctg gtctgggtgta tgcaaattgt atggaaaaag 2008
ggctgtgtta atattcataa gaatacaaga acttaggaag agtgaggttg gtgtgtcact 2068
ggtcaacctt tgtgtcctcca gatcccatca cagtttggcg attgtggagg gcctcctgaa 2128
ggaggagatg agtaaataata tttttttgga gacagggctc cactgtgttg cccaggctgg 2188
agtgcagtag tgcagtcgtg gctcactgca gcctccacct cctgggctct ccagcgatct 2248
tcccacatca gcctcccgag tagctgggac cacaatgtg agcccacca tgcctggcta 2308
atttttgtac tttttgtata aatggagtct cactatgttt cccaggctg atcttgaact 2368
cctgggctca agagatcctc ctgccttggc ctcccaaagt gctcagatta gagatgtgag 2428
ccgccatgtc tggccagata aattaagtca aacatttggg ttccagaaaa taaagacaaa 2488
tagagaaggt tagatTTTTT tttttccaac aagtggataa aagtctgtga ctcgggggaa 2548
agtgaagga gaaatgcagc cgatatagag tcattatgtt tgcaaagccc ctgggtcatac 2608
aggccaggga acataagacc gcaattctaa gtttctagat aaacagcgat ctccaagtca 2668
agactgagga tgaagaggga gaatgtcaga actcaagtga agggcaatca gggcagactg 2728
cctggaggag tgatgccaga aggtttggga agaaggtgtg ggacaagaag aaagggtatt 2788
tattcattca ttcaacagag gtttatgtag ggcactgtgc tgggtggggc tggggacaca 2848
acaatgactg aggcagcctg gccttgccct cacagggctc accatacaca agtaaataaa 2908
aaatatgtaa tgtttggaat tgct 2932
```

<210> 13

<211> 365

<212> PRT

<213> Mus musculus

<400> 13

Met Asp Asn Ser Thr Gly Thr Gly Glu Gly Cys His Val Asp Ser Arg

1

5

10

15

Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val

20

25

30

Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val

35

40

45

Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala

50	55	60
Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu		
65	70	75 80
His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly		
	85	90 95
Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys		
	100	105 110
Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala		
	115	120 125
Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp		
	130	135 140
Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu		
	145	150 155 160
Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met		
	165	170 175
Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe		
	180	185 190
Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg		
	195	200 205
Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile		
	210	215 220
Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala		
	225	230 235 240
Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg		
	245	250 255

Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser  
260 265 270

Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr  
275 280 285

Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His  
290 295 300

Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn  
305 310 315 320

Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr  
325 330 335

Gly Lys Ser Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
340 345 350

Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
355 360 365

<210> 14

<211> 1098

<212> DNA

<213> Mus musculus

<400> 14

atg gac aac agc acg ggc aca ggg gag ggc tgc cat gtg gac tct cga 48  
Met Asp Asn Ser Thr Gly Thr Gly Glu Gly Cys His Val Asp Ser Arg  
1 5 10 15

gtg gac cac ctc ttc cca cca tct ctc tac atc ttc gtc atc ggg gtg 96  
Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
20 25 30

ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgg cag gtg 144  
Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val

35	40	45	
cgc caa cac aat gag ctg ggc gtc tac ctg atg aac ttg agc att gca			192
Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala			
50	55	60	
gac ctg ctg tac atc tgc act ttg ccg ctg tgg gtc gac tac ttc ctc			240
Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu			
65	70	75	80
cac cat gac aac tgg atc cac ggc cct ggc tcc tgc aag ctc ttt ggc			288
His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly			
	85	90	95
ttc atc ttc tac agc aac atc tat atc agc atc gcc ttc ctg tgc tgc			336
Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys			
	100	105	110
atc tcc gtg gac cgc tac ctg gct gtg gct cat cct ctg cgc ttt gca			384
Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala			
	115	120	125
cgc ctg cgc cgg gtc aag aca gca gtg gct gtg agc tct gtg gtc tgg			432
Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp			
130	135	140	
gcc acg gag ctg ggc gcc aat tca gca ccg ctc ttc cat gat gag ctg			480
Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu			
145	150	155	160
ttt cgt gat cgc tac aac cac acc ttc tgc ttt gag aag ttc ccc atg			528
Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met			
	165	170	175
gag cgt tgg gtg gcc tgg atg aat ctg tac cgc gtc ttt gtg ggc ttc			576
Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe			
	180	185	190

ctc ttc ccc tgg gca ctc atg ttg ctg tgc tac cgt ggc atc ctg agg	624
Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg	
195 200 205	
gca gtg cag agc agt gtg tcc acc gag cgc cag gag aaa gtc aag atc	672
Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile	
210 215 220	
aaa cgt ctg gcc ctg agc ctc atc gcc att gtg ctg gtg tgc ttt gcg	720
Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala	
225 230 235 240	
cct tac cat gct ctc ctg ctg tct cgc agc gcc gtc tac ctg ggc cgg	768
Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg	
245 250 255	
ccc tgg gac tgt ggc ttc gag gag cga gtc ttt tct gcc tac cac agc	816
Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser	
260 265 270	
tcc ctg gcc ttc acc agc ctc aat tgt gtg gct gac ccc atc ctc tac	864
Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr	
275 280 285	
tgc ctg gtc aac gag ggt gcc cgc agt gat gtg gcc aag gcc ctg cac	912
Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His	
290 295 300	
aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat	960
Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn	
305 310 315 320	
gct tcc ctc acc ctg gag aca ccc ttg acc tcc aag agg agc acc acc	1008
Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr	
325 330 335	
ggc aag tcg tcc ggg gct gtc tgg gca gtg cct ccg act gcc cag ggg	1056
Gly Lys Ser Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly	

340	345	350	
gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga			1098
Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln			
355	360	365	

<210> 15  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: synthetic DNA

<400> 15	
ataagcttgac caccatggac aacagcacgg gcac	34

<210> 16  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: synthetic DNA

<400> 16	
tagcggccgc tcactgtgcc gggggcagca g	31

<210> 17  
 <211> 365  
 <212> PRT  
 <213> Rattus norvegicus

<400> 17	
Met Asp Asn Ser Thr Gly Thr Trp Glu Gly Cys His Val Asp Ser Arg	
1                      5                      10                      15	

Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
20 25 30

Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
35 40 45

Arg Gln Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
50 55 60

Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu  
65 70 75 80

His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly  
85 90 95

Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys  
100 105 110

Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala  
115 120 125

Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp  
130 135 140

Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu  
145 150 155 160

Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met  
165 170 175

Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe  
180 185 190

Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg  
195 200 205

Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile  
210 215 220



Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala  
 225 230 235 240

Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg  
 245 250 255

Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser  
 260 265 270

Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr  
 275 280 285

Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His  
 290 295 300

Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn  
 305 310 315 320

Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr  
 325 330 335

Gly Lys Thr Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
 340 345 350

Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
 355 360 365

<210> 18

<211> 1098

<212> DNA

<213> Rattus norvegicus

<400> 18

atg gac aac agc acg ggc acg tgg gag ggc tgc cat gtg gac tct cga  
 Met Asp Asn Ser Thr Gly Thr Trp Glu Gly Cys His Val Asp Ser Arg  
 1 5 10 15

gtg gac cac ctc ttc cca cca tcc ctc tac atc ttc gtc atc ggg gtg	96
Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val	
20 25 30	
ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgc cag gtg	144
Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val	
35 40 45	
cgc cag cgc aat gag ctg ggc gtc tac ctg atg aac ttg agc atc gca	192
Arg Gln Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala	
50 55 60	
gac ctg ctg tac atc tgt acg ctg ccg ctg tgg gtc gac tac ttc ctc	240
Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu	
65 70 75 80	
cac cat gac aac tgg atc cac ggc ccc ggc tcc tgc aag ctc ttt ggc	288
His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly	
85 90 95	
ttc atc ttc tac agc aac atc tac atc agc atc gcc ttc ctg tgc tgc	336
Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys	
100 105 110	
atc tcc gtg gac cgc tac ctg gct gtg gcc cat ccg ctg cgc ttt gcg	384
Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala	
115 120 125	
cgc ctg cgc cgg gtc aag aca gca gta gct gtg agc tcc gtg gtc tgg	432
Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp	
130 135 140	
gcc acc gag cta ggc gcc aac tcg gca ccg ctc ttt cat gac gag ctc	480
Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu	
145 150 155 160	
ttt cgt gat cgc tac aac cac acc ttc tgc ttc gag aag ttc ccc atg	528

Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met	
165 170 175	
gag cgc tgg gtg gcc tgg atg aac ctg tac cgc gtc ttt gtg ggg ttc	576
Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe	
180 185 190	
ctc ttc ccc tgg gca ctc atg ttg ctg tgc tac cgc ggc atc ctg cgg	624
Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg	
195 200 205	
gcc gta cag agc agt gtg tcc acc gag cgc cag gag aaa gtc aag atc	672
Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile	
210 215 220	
aaa cgc ctg gcc ctg agc ctc atc gcc atc gtg ctg gtg tgc ttt gca	720
Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala	
225 230 235 240	
ccc tac cat gct ctc ttg ctg tct cgc agc gct gtc tat ctg ggc cgg	768
Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg	
245 250 255	
ccc tgg gac tgt ggc ttc gag gag cga gtc ttc tct gcc tac cac agc	816
Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser	
260 265 270	
tcc cta gcc ttc acc agc ctc aat tgc gtg gct gac ccc atc ctc tac	864
Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr	
275 280 285	
tgc ctg gtc aac gag ggt gcc cgt agt gac gtg gcc aaa gcc ctg cac	912
Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His	
290 295 300	
aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat	960
Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn	
305 310 315 320	

gct tcc ctc acc ctg gag aca cca ttg acc tcc aag agg agc acc acc 1008  
Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr  
325 330 335

ggc aaa acg tct ggg gct gtc tgg gca gtg cct ccc act gcc cag ggg 1056  
Gly Lys Thr Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
340 345 350

gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga 1098  
Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
355 360 365